```
NEWS 12  Jun 28  Additional enzyme-catalyzed reactions added to CASREACT
NEWS 13  Jun 28  ANTE, AQUALINE, BIOENG, CIVILENG, ENVIROENG, MECHENG,
                 and WATER from CSA now available on STN(R)

NEWS EXPRESS  MARCH 31 CURRENT WINDOWS VERSION IS V7.00A, CURRENT
              MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
              AND CURRENT DISCOVER FILE IS DATED 26 APRIL 2004
NEWS HOURS    STN Operating Hours Plus Help Desk Availability
NEWS INTER    General Internet Information
NEWS LOGIN    Welcome Banner and News Items
NEWS PHONE    Direct Dial and Telecommunication Network Access to STN
NEWS WWW      CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that
specific topic.

  All use of STN is subject to the provisions of the STN Customer
  agreement.  Please note that this agreement limits use to scientific
  research.  Use for software development or design or implementation
  of commercial gateways or other similar uses is prohibited and may
  result in loss of user privileges and other penalties.

  * * * * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 16:49:57 ON 06 JUL 2004

=> FIL MEDLINE BIOSIS EMBASE CA SCISEARCH
COST IN U.S. DOLLARS                                  SINCE FILE      TOTAL
                                                        ENTRY     SESSION
FULL ESTIMATED COST                                      0.21        0.21

FILE 'MEDLINE' ENTERED AT 16:50:07 ON 06 JUL 2004

FILE 'BIOSIS' ENTERED AT 16:50:07 ON 06 JUL 2004
COPYRIGHT (C) 2004 BIOLOGICAL ABSTRACTS INC.(R)

FILE 'EMBASE' ENTERED AT 16:50:07 ON 06 JUL 2004
COPYRIGHT (C) 2004 Elsevier Inc. All rights reserved.

FILE 'CA' ENTERED AT 16:50:07 ON 06 JUL 2004
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2004 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'SCISEARCH' ENTERED AT 16:50:07 ON 06 JUL 2004
COPYRIGHT 2004 THOMSON ISI

=> s intron?
L1       147606 INTRON?

=> s foreign or introduc? or insert? or non-native? or sv40?
L2      2099538 FOREIGN OR INTRODUC? OR INSERT? OR NON-NATIVE? OR SV40?

=> s l1 (3n) l2
L3         4427 L1 (3N) L2

=> s (nuclei? acid) or sequence or (vector (2N) contain?) OR cDNA or (coding
sequence)
   4 FILES SEARCHED...
L4      3384674 (NUCLEI? ACID) OR SEQUENCE OR (VECTOR (2N) CONTAIN?) OR CDNA OR
                (CODING SEQUENCE)

=> s l1 (3n) l2 (3n) l3
L5          180 L1 (3N) L2 (3N) L3
```

```
=> s l1 (2n) l2 (2n) l3
L6          178 L1 (2N) L2 (2N) L3

=> s l6 (2n) polymeras?
L7            0 L6 (2N) POLYMERAS?

=> d l6 1-10 ibib abs

L6   ANSWER 1 OF 178     MEDLINE on STN
ACCESSION NUMBER:    2003336286     MEDLINE
DOCUMENT NUMBER:     PubMed ID: 12868603
TITLE:               Introns in gene evolution.
AUTHOR:              Fedorova Larisa; Fedorov Alexei
CORPORATE SOURCE:    Vision Research Laboratories, New England Medical Center,
                     Tufts University School of Medicine, Boston, MA 02111,
                     USA.. lfedorova@lifespan.org
SOURCE:              Genetica, (2003 Jul) 118 (2-3) 123-31.  Ref: 95
                     Journal code: 0370740. ISSN: 0016-6707.
PUB. COUNTRY:        Netherlands
DOCUMENT TYPE:       Journal; Article; (JOURNAL ARTICLE)
                     General Review; (REVIEW)
                     (REVIEW, TUTORIAL)
LANGUAGE:            English
FILE SEGMENT:        Priority Journals
ENTRY MONTH:         200309
ENTRY DATE:          Entered STN: 20030719
                     Last Updated on STN: 20030913
                     Entered Medline: 20030912
AB   Introns are integral elements of eukaryotic genomes that perform various
     important functions and actively participate in gene evolution.  We review
     six distinct roles of spliceosomal introns: (1) sources of non-coding RNA;
     (2) carriers of transcription regulatory elements; (3) actors in
     alternative and trans-splicing; (4) enhancers of meiotic crossing over
     within coding sequences; (5) substrates for exon shuffling; and (6)
     signals for mRNA export from the nucleus and nonsense-mediated decay.  We
     consider transposable capacities of introns and the current state of the
     long-lasting debate on the 'early-or-late' origin of introns.  Cumulative
     data on known types of contemporary exon shuffling and the estimation of
     the size of the underlying exon universe are also discussed.  We argue
     that the processes central to introns-early (exon shuffling) and
     introns-late (intron insertion) theories are
     entirely compatible.  Each has provided insight: the latter through
     elucidating the transposon capabilities of introns, and the former through
     understanding the importance of introns in genomic recombination leading
     to gene rearrangements and evolution.

L6   ANSWER 2 OF 178     MEDLINE on STN
ACCESSION NUMBER:    2003256655     MEDLINE
DOCUMENT NUMBER:     PubMed ID: 12781137
TITLE:               Importance of a single base pair for discrimination between
                     intron-containing and intronless alleles by endonuclease
                     I-BmoI.
AUTHOR:              Edgell David R; Stanger Matthew J; Belfort Marlene
CORPORATE SOURCE:    Molecular Genetics Program, Wadsworth Center, New York
                     State Department of Health, P.O. Box 22002, Albany, NY
                     12201-2002, USA.. edgell@wadsworth.org
CONTRACT NUMBER:     GM39422 (NIGMS)
     GM44844 (NIGMS)
SOURCE:              Current biology : CB, (2003 May 27) 13 (11) 973-8.
                     Journal code: 9107782. ISSN: 0960-9822.
PUB. COUNTRY:        England: United Kingdom
DOCUMENT TYPE:       Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:            English
```

FILE SEGMENT: Priority Journals
ENTRY MONTH: 200403
ENTRY DATE: Entered STN: 20030604
Last Updated on STN: 20040306
Entered Medline: 20040305

AB Homing endonucleases initiate mobility of their host group I introns by binding to and cleaving lengthy recognition sequences that are typically centered on the **intron insertion** site (IS) of **intronless** alleles. Because the intron interrupts the endonucleases' recognition sequence, intron-containing alleles are immune to cleavage by their own endonuclease. I-TevI and I-BmoI are related GIY-YIG endonucleases that bind a homologous stretch of thymidylate synthase (TS)-encoding DNA but use different strategies to distinguish intronless from intron-containing substrates. I-TevI discriminates between substrates at the level of DNA binding, as its recognition sequence is centered on the intron IS. I-BmoI, in contrast, possesses a very asymmetric recognition sequence with respect to the intron IS, binds both intron-containing and intronless TS-encoding substrates, but efficiently cleaves only intronless substrate. Here, we show that I-BmoI is extremely tolerant of multiple substitutions around its cleavage sites and has a low specific activity. However, a single G-C base pair, at position -2 of a 39-base pair recognition sequence, is a major determinant for cleavage efficiency and distinguishes intronless from intron-containing alleles. Strikingly, this G-C base pair is universally conserved in phylogenetically diverse TS-coding sequences; this finding suggests that I-BmoI has evolved exquisite cleavage requirements to maximize the potential to spread to variant intronless alleles, while minimizing cleavage at its own intron-containing allele.

L6 ANSWER 3 OF 178 MEDLINE on STN
ACCESSION NUMBER: 2001688502 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11734905
TITLE: Dynamic insertion-deletion of introns in deuterostome EF-1alpha genes.
AUTHOR: Wada Hiroshi; Kobayashi Mari; Sato Riki; Satoh Nori; Miyasaka Hitoshi; Shirayama Yoshihisa
CORPORATE SOURCE: Seto Marine Biological Laboratory, Graduate School of Sciences, Kyoto University, 459 Shirahama, Wakayama, 649-2211, Japan.. hwada@seto.kyoto-u.ac.jp
SOURCE: Journal of molecular evolution, (2002 Jan) 54 (1) 118-28. Journal code: 0360051. ISSN: 0022-2844.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB070229; GENBANK-AB070230; GENBANK-AB070231; GENBANK-AB070232; GENBANK-AB070233; GENBANK-AB070234; GENBANK-AB070235
ENTRY MONTH: 200208
ENTRY DATE: Entered STN: 20011206
Last Updated on STN: 20020816
Entered Medline: 20020815

AB To test the validity of intron-exon structure as a phylogenetic marker, the intron-exon structure of EF-1alpha genes was investigated for starfish, acornworms, ascidians, larvaceans, and amphioxus and compared with that of vertebrates. Of the 11 distinct intron insertion sites found within the coding regions of the deuterostome EF-1alpha genes, 7 are shared by several taxa, while the remainder are unique to certain taxa. Examination of the shared introns of the deuterostome EF-1alpha gene revealed that independent **intron** loss or **intron insertion** must have occurred in separate lineages of the deuterostome taxa. Maximum parsimony analysis of the intron-exon data matrix recovered five parsimonious trees (consistency index = 0.867). From this result, we concluded that the intron-exon structure of

deuterostome EF-1alpha has evolved more dynamically than previously thought, rendering it unsuitable as a phylogenetic marker. We also reconstructed an evolutionary history of intron insertion-deletion events on the deuterostome phylogeny, based on several molecular phylogenetic studies. These analyses revealed that the deuterostome EF-1alpha gene has lost individual introns more frequently than all introns simultaneously.

L6 ANSWER 4 OF 178 MEDLINE on STN
ACCESSION NUMBER: 2001385026 MEDLINE
DOCUMENT NUMBER: PubMed ID: 11416170
TITLE: Related homing endonucleases I-BmoI and I-TevI use different strategies to cleave homologous recognition sites.
AUTHOR: Edgell D R; Shub D A
CORPORATE SOURCE: Department of Biological Sciences and Center for Molecular Genetics, State University of New York, Albany, NY 12222, USA.
CONTRACT NUMBER: GM37746 (NIGMS)
GM44844 (NIGMS)
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (2001 Jul 3) 98 (14) 7898-903. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF321518
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010813
Last Updated on STN: 20030105
Entered Medline: 20010809

AB A typical homing endonuclease initiates mobility of its group I intron by recognizing DNA both upstream and downstream of the **intron insertion** site of **intronless** alleles, preventing the endonuclease from binding and cleaving its own intron-containing allele. Here, we describe a GIY-YIG family homing endonuclease, I-BmoI, that possesses an unusual recognition sequence, encompassing 1 base pair upstream but 38 base pairs downstream of the intron insertion site. I-BmoI binds intron-containing and intronless substrates with equal affinity but can nevertheless discriminate between the two for cleavage. I-BmoI is encoded by a group I intron that interrupts the thymidylate synthase (TS) gene (thyA) of Bacillus mojavensis s87-18. This intron resembles one inserted 21 nucleotides further downstream in a homologous TS gene (td) of Escherichia coli phage T4. I-TevI, the T4 td intron-encoded GIY-YIG endonuclease, is very similar to I-BmoI, but each endonuclease gene is inserted within a different position of its respective intron. Remarkably, I-TevI and I-BmoI bind a homologous stretch of TS-encoding DNA and cleave their intronless substrates in very similar positions. Our results suggest that each endonuclease has independently evolved the ability to distinguish intron-containing from intronless alleles while maintaining the same conserved recognition sequence centered on DNA-encoding active site residues of TS.

L6 ANSWER 5 OF 178 MEDLINE on STN
ACCESSION NUMBER: 2000132412 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10668928
TITLE: Normolipidemia and hypercholesterolemia in persons heterozygous for the same 1592 + 5G --> A splice site mutation in the low-density lipoprotein receptor gene.
AUTHOR: Jensen H K; Jensen L G; Holst H U; Andreasen P H; Hansen P S; Larsen M L; Kolvraa S; Bolund L; Gregersen N; Faergeman O
CORPORATE SOURCE: Department of Medicine and Cardiology, Aarhus Amtssygehus University Hospital, Denmark.. hkjensen@dadlnet.dk

SOURCE: Clinical genetics, (1999 Nov) 56 (5) 378-88.
Journal code: 0253664. ISSN: 0009-9163.
PUB. COUNTRY: Denmark
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200002
ENTRY DATE: Entered STN: 20000314
Last Updated on STN: 20000314
Entered Medline: 20000225

AB In the present study, we have characterized a unique splice donor G to A substitution in the moderately conserved + 5 position in intron 10 of the low-density lipoprotein (LDL) receptor gene. In two Danish families, carriers of the 1592 + 5G --> A mutation display a clinical phenotype ranging from healthy normocholesterolemic persons to classical heterozygous familial hypercholesterolemia (FH) patients. Reverse transcription-polymerase chain reaction (RT-PCR) of RNA from Epstein Barr virus (EBV)-transformed lymphoblasts obtained from members of both families demonstrated abnormal splicing generating two aberrant mRNAs due to either alternative splicing and skipping of exon 10 or activation of a cryptic splice site in **intron** 10 **inserting** 66 **intronic** base pairs. These abnormally spliced mRNAs were predicted to encode two abnormal receptor proteins containing an in-frame deletion of 75 amino acids and an insertion of 22 novel amino acids, respectively. Results obtained by immunofluorescence staining, flow cytometry, and confocal microscopy of transfected Chang and COS-7 cells expressing normal and mutant LDL receptors were compatible with nearly complete retention of the mutant proteins in the endoplasmic reticulum. Quantitative measurements of LDL receptor mRNAs from EBV-transformed lymphoblasts, however, did not reveal any significant differences in variant mRNA contents between mutation carriers in the families that could be related to degree of hypercholesterolemia.

L6 ANSWER 6 OF 178 MEDLINE on STN
ACCESSION NUMBER: 2000131357 MEDLINE
DOCUMENT NUMBER: PubMed ID: 10666705
TITLE: A diverse population of introns in the nuclear ribosomal genes of ericoid mycorrhizal fungi includes elements with sequence similarity to endonuclease-coding genes.
AUTHOR: Perotto S; Nepote-Fus P; Saletta L; Bandi C; Young J P
CORPORATE SOURCE: Centro Studio Micologia del Terreno-CNR, Torino, Italy.. perotto@bioveg.unito.it
SOURCE: Molecular biology and evolution, (2000 Jan) 17 (1) 44-59.
Journal code: 8501455. ISSN: 0737-4038.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200002
ENTRY DATE: Entered STN: 20000309
Last Updated on STN: 20000309
Entered Medline: 20000222

AB Ericoid mycorrhizal fungi form symbioses with the roots of members of the Ericales. Although only two genera have been identified in culture, the taxonomic diversity of ericoid symbionts is certainly wider. Genetic variation among 40 ericoid fungal isolates was investigated in this study. PCR amplification of the nuclear small-subunit ribosomal DNA (SSU rDNA) and of the internal transcribed spacer (ITS), followed by sequencing, led to the discovery of DNA insertions of various sizes in the SSU rDNA of most isolates. They reached sizes of almost 1,800 bp and occurred in up to five different insertion sites. Their positions and sizes were generally correlated with morphological and ITS-RFLP grouping of the isolates, although some insertions were found to be optional among isolates of the same species, and insertions were not always present in

all SSU rDNA repeats within an isolate. Most insertions were identified as typical group I introns, possessing the conserved motifs characteristic of this group. However, other insertions lack these motifs and form a distinct group that includes other fungal ribosomal introns. Alignments with almost 70 additional sequences from fungal nuclear SSU rDNA **introns** indicate that **introns inserted** at the same site along the rDNA gene are generally homologous, but they also suggest the possibility of some horizontal transfers. Two of the ericoid fungal introns showed strong homology with a conserved motif found in endonuclease genes from nuclear rDNA introns.

L6 ANSWER 7 OF 178 MEDLINE on STN
ACCESSION NUMBER: 1998316784 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9654212
TITLE: The effects of splice site mutations in patients with naevoid basal cell carcinoma syndrome.
AUTHOR: Smyth I; Wicking C; Wainwright B; Chenevix-Trench G
CORPORATE SOURCE: Centre for Molecular and Cellular Biology, Ritchie Research Laboratories, University of Queensland, Australia.
SOURCE: Human genetics, (1998 May) 102 (5) 598-601. Journal code: 7613873. ISSN: 0340-6717.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199807
ENTRY DATE: Entered STN: 19980723
Last Updated on STN: 19980723
Entered Medline: 19980716

AB We have previously identified the human homologue of the Drosophila patched gene and have described, in this gene, mutations that give rise to naevoid basal cell carcinoma syndrome (NBCCS). Here, we have analysed the effects of three splice site mutations within human PATCHED (PTCH) by the reverse transcription/polymerase chain reaction method in cultured patient lymphocyte cell lines. Two alterations, a point mutation in **intron** 7 and an **insertion** in **intron** 10, lead to premature truncation of the PATCHED protein. Another point mutation in intron 17 results in the skipping of exon 18 and the subsequent in-frame deletion of 46 amino acids. Additionally, in all lymphocyte and keratinocyte cell lines examined, exon 10 of PTCH is alternatively spliced leading to an in-frame deletion of 52 amino acids.

L6 ANSWER 8 OF 178 MEDLINE on STN
ACCESSION NUMBER: 1998132646 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9465071
TITLE: De novo insertion of an intron into the mammalian sex determining gene, SRY.
AUTHOR: O'Neill R J; Brennan F E; Delbridge M L; Crozier R H; Graves J A
CORPORATE SOURCE: School of Genetics and Human Variation, La Trobe University, Bundoora, VIC 3083, Australia.. racho@princeton.edu
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, (1998 Feb 17) 95 (4) 1653-7. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF005509; GENBANK-AF005510; GENBANK-AF005511
ENTRY MONTH: 199803
ENTRY DATE: Entered STN: 19980326
Last Updated on STN: 19980326
Entered Medline: 19980319

AB Two theories have been proposed to explain the evolution of introns within eukaryotic genes. The introns early theory, or "exon theory of genes," proposes that introns are ancient and that recombination within introns provided new exon structure, and thus new genes. The **introns** late theory, or "**insertional** theory of **introns**," proposes that ancient genes existed as uninterrupted exons and that introns have been introduced during the course of evolution. There is still controversy as to how intron-exon structure evolved and whether the majority of introns are ancient or novel. Although there is extensive evidence in support of the introns early theory, phylogenetic comparisons of several genes indicate recent gain and loss of introns within these genes. However, no example has been shown of a protein coding gene, intronless in its ancestral form, which has acquired an intron in a derived form. The mammalian sex determining gene, SRY, is intronless in all mammals studied to date, as is the gene from which it recently evolved. However, we report here comparisons of genomic and cDNA sequences that now provide evidence of a de novo insertion of an intron into the SRY gene of dasyurid marsupials. This recently (approximately 45 million years ago) inserted sequence is not homologous with known transposable elements. Our data demonstrate that introns may be inserted as spliced units within a developmentally crucial gene without disrupting its function.

L6 ANSWER 9 OF 178 MEDLINE on STN
ACCESSION NUMBER: 1998117314 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9458110
TITLE: Screening of the TAP1 gene by denaturing gradient gel electrophoresis in insulin-dependent diabetes mellitus: detection and comparison of new polymorphisms between patients and controls.
AUTHOR: Yan G; Shi L; Fu Y; Wang X; Schoenfeld D; Ma L; Penfornis A; Gebel H; Faustman D L
CORPORATE SOURCE: Immunobiology Laboratory, Massachusetts General Hospital, Charlestown 02129, USA.
CONTRACT NUMBER: P30-DK40561 (NIDDK)
R01 DE11151-03 (NIDCR)
R03-DE11023-02 (NIDCR)
SOURCE: Tissue antigens, (1997 Dec) 50 (6) 576-85.
Journal code: 0331072. ISSN: 0001-2815.
PUB. COUNTRY: Denmark
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199803
ENTRY DATE: Entered STN: 19980326
Last Updated on STN: 20030110
Entered Medline: 19980313

AB New protective or disease-associated polymorphisms in the TAP1 gene were sought in insulin-dependent diabetes mellitus (IDDM) patients with the use of denaturing gradient gel electrophoresis (DGGE) screening of genomic DNA. The TAP1 gene is located in the human leukocyte antigen (HLA) class II region of the genome and encodes components of a peptide transporter essential for antigen presentation by HLA class I molecules. Fragments of TAP1 corresponding to the 5' promoter, each of the 11 exons (with portions of adjacent intronic regions) and the 3' flanking region were amplified by the polymerase chain reaction and then subjected to DGGE. DNA fragments of TAP1 yielded DGGE bands with patterns whose frequencies differed between IDDM patients and controls. Specific DGGE band patterns with fragments corresponding to the promoter, exons or introns 3, 6, 7, 8, 9 or 10 of TAP1 were detected exclusively in either patients or controls. Sequencing of TAP1 fragments encompassing exon 7 gave rise to a DGGE band pattern exclusively observed in an IDDM patient and sequencing revealed a previously unidentified polymorphisms at codon 518 (GTC-->ATC, Val-->Ile). Another unique polymorphism uncovered by DGGE revealed by sequencing a

polymorphism in intron 2 in a diabetic patient. The genotypes of additional HLA class II matched patients and controls were determined with regard to five exonic and one intronic TAP1 polymorphism. A 10 base pair **intronic insertion** in **intron** 9 was exclusively identified in controls and missing from patients (P = 0.017). Further large population-based studies may reveal whether these newly identified at risk or protective TAP1 variants confer markers of statistical risk in diverse population groups.

L6 ANSWER 10 OF 178 MEDLINE on STN
ACCESSION NUMBER: 97320631 MEDLINE
DOCUMENT NUMBER: PubMed ID: 9177482
TITLE: Cloning of two splicing variants of the novel Ras-related GTPase Rab29 which is predominantly expressed in kidney.
AUTHOR: Massmann S; Schurmann A; Joost H G
CORPORATE SOURCE: Institut fur Pharmakologie und Toxikologie, Medizinische Fakultat derRWTH Aachen, Germany.
SOURCE: Biochimica et biophysica acta, (1997 May 2) 1352 (1) 48-55. Journal code: 0217513. ISSN: 0006-3002.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M94043; GENBANK-X96663
ENTRY MONTH: 199706
ENTRY DATE: Entered STN: 19970709
Last Updated on STN: 20000303
Entered Medline: 19970625

AB cDNA of a novel Ras-related GTP-binding protein was isolated from rat tissue by a PCR-based cloning approach, and was designated Rab29 because its deduced amino acid sequence (204 aa) is remotely similar to that of members of the Rab family (30% identity with Rab1). mRNA of Rab29 was found predominately in kidney. Recombinant Rab29 exhibited rapid exchange of bound guanine nucleotides for radiolabeled GTP but lacked a detectable intrinsic GTPase activity. A second cDNA clone was isolated which contained a 287 bp in-frame insertion with characteristics of an **intron** sequence; this **insertion introduces** a stop codon after arginine 167. The recombinant protein (Rab29delta37) derived from the cDNA carrying the insertion was loaded with GTP during biosynthesis, but showed almost no exchange of the nucleotide for radiolabeled GTP. Thus, the C-terminus of Rab29 appears to harbor a structural element which is essential for the nucleotide exchange of the protein.

=> d his

(FILE 'HOME' ENTERED AT 16:49:57 ON 06 JUL 2004)

FILE 'MEDLINE, BIOSIS, EMBASE, CA, SCISEARCH' ENTERED AT 16:50:07 ON 06 JUL 2004

L1 147606 S INTRON?
L2 2099538 S FOREIGN OR INTRODUC? OR INSERT? OR NON-NATIVE? OR SV40?
L3 4427 S L1 (3N) L2
L4 3384674 S (NUCLEI? ACID) OR SEQUENCE OR (VECTOR (2N) CONTAIN?) OR CDNA
L5 180 S L1 (3N) L2 (3N) L3
L6 178 S L1 (2N) L2 (2N) L3
L7 0 S L6 (2N) POLYMERAS?

=> dup rem l6
PROCESSING COMPLETED FOR L6
L8 85 DUP REM L6 (93 DUPLICATES REMOVED)

=> s l8 and Py<=1995

```
   2 FILES SEARCHED...
L9          23 L8 AND PY<=1995

=> s l1 (3n) l2 (3n) l4
L10        558 L1 (3N) L2 (3N) L4

=> s l10 and polymeras?
L11        116 L10 AND POLYMERAS?

=> s l10 (3n) polymeras?
L12          0 L10 (3N) POLYMERAS?

=> s l10 (s) polymeras?
L13         28 L10 (S) POLYMERAS?

=> dup rem l13
PROCESSING COMPLETED FOR L13
L14          16 DUP REM L13 (12 DUPLICATES REMOVED)

=> s l14 and py=<1995
   2 FILES SEARCHED...
L15          5 L14 AND PY=<1995

=> d l15 ibib abs 1-5

L15  ANSWER 1 OF 5     MEDLINE on STN
ACCESSION NUMBER:    90232359     MEDLINE
DOCUMENT NUMBER:     PubMed ID: 2158670
TITLE:               RNA polymerase II transcription blocked by Escherichia coli
                     lac repressor.
AUTHOR:              Deuschle U; Hipskind R A; Bujard H
CORPORATE SOURCE:    Zentrum fur Molekulare Biologie, Universitat Heidelberg,
                     Federal Republic of Germany.
SOURCE:              Science, (1990 Apr 27) 248 (4954) 480-3.
                     Journal code: 0404511. ISSN: 0036-8075.
PUB. COUNTRY:        United States
DOCUMENT TYPE:       Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:            English
FILE SEGMENT:        Priority Journals
ENTRY MONTH:         199005
ENTRY DATE:          Entered STN: 19900706
                     Last Updated on STN: 19900706
                     Entered Medline: 19900525
AB   A reversible block to RNA polymerase II transcriptional
     elongation has been created with a lac operator sequence in the
     intron of the SV40 large T-antigen gene. When this
     transcription unit is injected into rabbit kidney cells expressing
     Escherichia coli lac repressor, T-antigen expression is reduced. This
     effect is not observed in cells lacking repressor or in the absence of the
     operator, and it is reversed by an inducer of the lac operon, namely
     isopropyl thiogalactoside (IPTG). In an extract of HeLa nuclei
     supplemented with lac repressor, this and similar constructs give rise to
     shortened transcripts that map to the 5' boundary of the
     repressor-operator complex. These shorter RNAs are also sensitive to IPTG
     induction. This model system shows that a protein-DNA complex can block
     the passage of RNA polymerase II, and offers some insight into the control
     of eukaryotic gene expression during transcription elongation, a
     phenomenon observed in a variety of systems.

L15  ANSWER 2 OF 5  EMBASE  COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.
     on STN
ACCESSION NUMBER:    95116730  EMBASE
DOCUMENT NUMBER:     1995116730
TITLE:               Human ferrochelatase: A novel mutation in patients with
```

erythropoietic protoporphyria and an isoform caused by alternative splicing.

AUTHOR: Schneider-Yin X.; Schafer B.W.; Tonz O.; Minder E.I.

CORPORATE SOURCE: Zentrallabor, Stadtspital Triemli, Birmensdorferstrasse 497,CH-8063 Zurich, Switzerland

SOURCE: Human Genetics, (1995) 95/4 (391-396).
ISSN: 0340-6717 CODEN: HUGEDQ

COUNTRY: Germany

DOCUMENT TYPE: Journal; Article

FILE SEGMENT: 013 Dermatology and Venereology
022 Human Genetics
029 Clinical Biochemistry

LANGUAGE: English

SUMMARY LANGUAGE: English

AB Erythropoietic protoporphyria (EPP), attributable to deficiency of ferrochelatase activity (FECH), is characterised mainly by cutaneous photosensitivity. To define the molecular defect in two EPP-affected siblings and their parents in a Swiss family, ferrochelatase cDNA was amplified by the **polymerase** chain reaction (PCR) and subjected to sequence analysis. A 5-bp deletion (T580-G584) was identified on one allele of the ferrochelatase gene in both patients and their mother. Screening of the mutation among family members by RsaI digestion of PCR-amplified genomic DNA revealed autosomal dominant inheritance associated with abnormal protoporphyrin concentration and enzyme activity. We also isolated ferrochelatase cDNAs containing a 18-bp **insertion** (part of the **intron** 2 **sequence**) between exons 2 and 3; this corresponded to six extra amino acids (YESNIR) inserted between Arg-65 and Lys-66 of the known ferrochelatase. This isoform was identified initially in mRNAs derived from both alleles of the ferrochelatase gene in one patient. Its existence was confirmed in six additional EPP patients, in five out of seven controls, and in four different cell lines (fibroblast, muscle, hepatoma and myelogenous leukaemia). This isoform, roughly 20% of the total ferrochelatase mRNA, was generated through splicing at a second donor site in intron 2 and its presence was not linked to EPP.

L15 ANSWER 3 OF 5 EMBASE
on STN

ACCESSION NUMBER: 94094036 EMBASE

DOCUMENT NUMBER: 1994094036

TITLE: Multiple group II self-splicing introns in mobile DNA from Escherichia coli.

AUTHOR: Ferat J.-L.; Le Gouar M.; Michel F.

CORPORATE SOURCE: Centre de Genetique Moleculaire, CNRS, Universite Pierre-et-Marie-Curie,91198 Gif-sur-Yvette, France

SOURCE: Comptes Rendus de l'Academie des Sciences - Serie III, (1994) 317/2 (141-148).
ISSN: 0764-4469 CODEN: CRASEV

COUNTRY: France

DOCUMENT TYPE: Journal; Article

FILE SEGMENT: 004 Microbiology

LANGUAGE: English

SUMMARY LANGUAGE: English; French

AB By PCR (**polymerase** chain reaction) amplification and cloning, we have identified four group II self-splicing introns encoding proteins related to reverse transcriptases in natural Escherichia coli isolates belonging to the ECOR collection. One intron, IntD, interrupts a DNA sequence virtually identical to that of the previously described IS3411 **Insertion Sequence.** A second **intron**, IntC, is located within an open reading frame that is closely related to a reading frame in the T-DNA of Agrobacterium tumefaciens. Finally, introns IntA and IntB are inserted at two distinct sites in one of the Rhs elements of E. coli. A comparison of their open reading frames shows that the two Rhs introns are more closely related to each other than to any other known

group II intron: this suggests that transposition of group II introns may occur preferentially in cis, along the same piece of DNA.

L15 ANSWER 4 OF 5 CA COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 116:35640 CA
TITLE: New diagnostic and treatment methods involving the cystic fibrosis transmembrane regulator
INVENTOR(S): Gregory, Richard J.; Cheng, Seng H.; Smith, Alan; Paul, Sucharita; Hehir, Kathleen M.; Marshall, John
PATENT ASSIGNEE(S): Genzyme Corp., USA
SOURCE: Eur. Pat. Appl., 49 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 7
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 446017	A1	19910911	EP 1991-301819	19910305 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE				
CA 2037478	AA	19910906	CA 1991-2037478	19910304 <--
JP 06303978	A2	19941101	JP 1991-38810	19910305 <--
US 5981714	A	19991109	US 1996-691605	19960815
US 5750571	A	19980512	US 1996-774127	19961223
US 2002164782	A1	20021107	US 2000-568756	20000511
AU 765709	B2	20030925	AU 2000-53512	20000821
US 2003147854	A1	20030807	US 2002-161539	20020603

PRIORITY APPLN. INFO.:

US 1990-488307	A	19900305
US 1990-589295	A	19900927
US 1990-613592	A	19901115
US 1992-935603	B2	19920826
US 1992-985478	B2	19921203
US 1993-72708	A1	19930607
US 1993-87132	A2	19930702
AU 1997-43655	A3	19971031
US 1998-114950	B1	19980827
US 1999-248026	A1	19990210
US 2000-568756	B1	20000511

AB A cDNA for the complete human cystic fibrosis transmembrane conductance regulator (CFTCR) is provided. A method for stabilizing CFTER clones comprises placing it in a low-copy number plasmid, **inserting** an **intron** into the **coding sequence**, and/or altering the sequence to remove cryptic RNA **polymerase** promoter sequences. The CFTCR cDNA can be used to produce the CFTCR, to treat cystic fibrosis, to prepare transgenic animals, and to diagnose CFTCR dysfunction. Many mutations known to occur in cystic fibrosis patients were introduced into CFTCR cDNA, and this mutant cDNA was expressed in COS-7 cells. The mutations Δ phenylalanine-508, Δ isoleucine-507, lysine-464 changes to methionine, phenylalanine-508 changed to arginine, and serine-549 changed to isoleucine resulted in production of unstable, incompletely glycosylated CFTCR.

L15 ANSWER 5 OF 5 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
ACCESSION NUMBER: 94:97985 SCISEARCH
THE GENUINE ARTICLE: MU600
TITLE: EFFECT OF ARTIFICIALLY INSERTED INTRON ON GENE-EXPRESSION IN SACCHAROMYCES-CEREVISIAE
AUTHOR: YOSHIMATSU T (Reprint); NAGAWA F
CORPORATE SOURCE: WAKUNAGA PHARMACEUT CO LTD, INST BIOTECHNOL RES, MOLEC BIOL SECT, HIROSHIMA 72964, JAPAN (Reprint)
COUNTRY OF AUTHOR: JAPAN
SOURCE: DNA AND CELL BIOLOGY, (**JAN 1994**) Vol. 13, No. 1, pp. 51-58.

ISSN: 1044-5498.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 25

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The intron of the yeast RP51A gene was cloned with precision using the **polymerase** chain reaction (PCR) amplification method, and then inserted into several different positions of the yeast URA3 gene as well as the PGK-lacZ fusion gene without introduction of additional exon sequences. Analysis of transcripts of these genes showed that an intron inserted near the transcription start site of the gene was spliced out efficiently, whereas the same **intron sequences inserted** 200 hp or further downstream of the start site were not, resulting in a reduced level of mRNA. These results explain why intron-containing genes in yeast usually have an intron near the 5' end.

```
=> d his

     (FILE 'HOME' ENTERED AT 16:49:57 ON 06 JUL 2004)

     FILE 'MEDLINE, BIOSIS, EMBASE, CA, SCISEARCH' ENTERED AT 16:50:07 ON 06
     JUL 2004
L1        147606 S INTRON?
L2       2099538 S FOREIGN OR INTRODUC? OR INSERT? OR NON-NATIVE? OR SV40?
L3          4427 S L1 (3N) L2
L4       3384674 S (NUCLEI? ACID) OR SEQUENCE OR (VECTOR (2N) CONTAIN?) OR CDNA
L5           180 S L1 (3N) L2 (3N) L3
L6           178 S L1 (2N) L2 (2N) L3
L7             0 S L6 (2N) POLYMERAS?
L8            85 DUP REM L6 (93 DUPLICATES REMOVED)
L9            23 S L8 AND PY<=1995
L10          558 S L1 (3N) L2 (3N) L4
L11          116 S L10 AND POLYMERAS?
L12            0 S L10 (3N) POLYMERAS?
L13           28 S L10 (S) POLYMERAS?
L14           16 DUP REM L13 (12 DUPLICATES REMOVED)
L15            5 S L14 AND PY=<1995

=> s l10 and (cell death or apoptos?)
L16            0 L10 AND (CELL DEATH OR APOPTOS?)

=> s l10 and (cell death or apoptos? or toxic? or kill? or inhib?)
   3 FILES SEARCHED...
L17           64 L10 AND (CELL DEATH OR APOPTOS? OR TOXIC? OR KILL? OR INHIB?)

=> s l10 (s) (cell death or apoptos? or toxic? or kill? or inhib?)
   3 FILES SEARCHED...
L18           26 L10 (S) (CELL DEATH OR APOPTOS? OR TOXIC? OR KILL? OR INHIB?)

=> dup rem l18
PROCESSING COMPLETED FOR L18
L19           12 DUP REM L18 (14 DUPLICATES REMOVED)

=> s l19 and py=<1995
   1 FILES SEARCHED...
   3 FILES SEARCHED...
L20            3 L19 AND PY=<1995

=> d l20 ibib abs

L20  ANSWER 1 OF 3      MEDLINE on STN
ACCESSION NUMBER:    96074813      MEDLINE
```

DOCUMENT NUMBER: PubMed ID: 7476922
TITLE: Inhibition of splicing of wild-type and mutated luciferase-adenovirus pre-mRNAs by antisense oligonucleotides.
AUTHOR: Hodges D; Crooke S T
CORPORATE SOURCE: Department of Anatomy and Neurobiology, University of California, Irvine 92717, USA.
SOURCE: Molecular pharmacology, **(1995 Nov)** 48 (5) 905-18.
Journal code: 0035623. ISSN: 0026-895X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199512
ENTRY DATE: Entered STN: 19960124
Last Updated on STN: 19970203
Entered Medline: 19951220

AB We report the construction, characterization, and use of luciferase reporters to test the ability of antisense oligonucleotides to **inhibit** RNA splicing. beta-Globin and adenovirus **introns** were **inserted** into a luciferase **cDNA**, and luciferase expression was analyzed in transiently transfected cells. The adenovirus reporter expressed large amounts of luciferase, but two beta-globin constructs were inactive. RNA analyses determined that the beta-globin pre-mRNAs were not spliced. Mutagenesis of the beta-globin 5' splice site, branchpoint, and 3' splice site sequences to the adenovirus intron sequences promoted maximal splicing and luciferase activity; reciprocal changes in all three elements of the adenovirus intron eliminated luciferase activity. Wild-type and 3' splice site mutated adenovirus reporters were used to determine the ability of phosphorothioate deoxy and 2' methoxy oligonucleotides to inhibit splicing. RNase H activating oligodeoxynucleotides were better inhibitors of wild-type adenovirus expression than were 2' methoxy analogues. However, 2' methoxy oligonucleotides specific for the branchpoint were more effective inhibitors of splicing of adenovirus transcript containing the beta-globin branchpoint and 3' splice site. We suggest that pre-mRNAs with weak splice sites are potential targets for oligonucleotides that inhibit splicing by occupancy rather than cleavage of the transcripts.

=> d l20 ibib abs 2-3

L20 ANSWER 2 OF 3 MEDLINE on STN
ACCESSION NUMBER: 90384817 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2169607
TITLE: A novel selection system for recombinational and mutational events within an intron of a eucaryotic gene.
AUTHOR: Porter T; Pennington S L; Adair G M; Nairn R S; Wilson J H
CORPORATE SOURCE: Verna and Marrs McLean Department of Biochemistry, Baylor College of Medicine, Houston, Texas 77030.
CONTRACT NUMBER: CA28711 (NCI)
GM38219 (NIGMS)
SOURCE: Nucleic acids research, **(1990 Sep 11)** 18 (17) 5173-80.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199010
ENTRY DATE: Entered STN: 19901122
Last Updated on STN: 19901122
Entered Medline: 19901024

AB In order to identify a poison sequence that might be useful in studying

illegitimate recombination of mammalian cell chromosomes, several DNA segments were tested for their ability to interfere with gene expression when placed in an intron. A tRNA gene and its flanking sequences (267 bp) were shown to inhibit SV40 plaque formation 100-fold, when inserted into the intron in the T-antigen gene. Similarly, when the same DNA segment was placed in the second intron of the adenosine phosphoribosyl transferase (APRT) gene from CHO cells, it inhibited transformation of APRT-CHO cells 500-fold. These two tests indicated that the 267-bp DNA segment contained a poison sequence. The poison sequence did not affect replication since the replication of poisoned SV40 genomes was complemented by viable SV40 genomes and poisoned APRT genes were stably integrated into cell chromosomes. Cleavage of the poison **sequence** in the **SV40** T-antigen **intron** by restriction enzymes indicated that the tRNA structural sequences and the 5' flanking sequences were not required for **inhibition** of SV40 plaque formation. Sequence analysis of viable mutant SV40, which arose after transfection of poisoned genomes, localized the poison sequence to a 35 bp segment immediately 3' of the tRNA structural sequences.

L20 ANSWER 3 OF 3 SCISEARCH COPYRIGHT 2004 THOMSON ISI on STN
ACCESSION NUMBER: 91:367192 SCISEARCH
THE GENUINE ARTICLE: FT393
TITLE: AVOIDANCE OF INTER-REPEAT RECOMBINATION BY SEQUENCE DIVERGENCE AND A MECHANISM OF NEUTRAL EVOLUTION
AUTHOR: RADMAN M (Reprint)
CORPORATE SOURCE: INST JACQUES MONOD, F-75251 PARIS 05, FRANCE (Reprint)
COUNTRY OF AUTHOR: FRANCE
SOURCE: BIOCHIMIE, (**1991**) Vol. 73, No. 4, pp. 357-361.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 21

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Eucaryotic genomes are loaded with diverse repeated sequences and are therefore threatened by rearrangements via inter-repeat crossovers and by gene-inactivating conversions between genes and their inactive pseudogenes. Such repeated DNA sequences are usually diverged and polymorphic. Sequence divergence by well-spread point mutations is a potent **inhibitor** of homologous recombination due to the loss of recombination initiation sites and to the editing of recombinational intermediates by the mismatch repair system. Evidence is reviewed suggesting that a germ line process can identify duplicated sequences by homologous pairing, modify them by methylation and mutate by C --> T transitions. Since this process requires a minimum contiguous homology that is larger than the average exon size, it is proposed that fragmentation by **intron inserts** protects the **coding sequences** from inactivation by homologous interactions with their pseudogene sequences.

=> d his

(FILE 'HOME' ENTERED AT 16:49:57 ON 06 JUL 2004)

FILE 'MEDLINE, BIOSIS, EMBASE, CA, SCISEARCH' ENTERED AT 16:50:07 ON 06 JUL 2004

L1 147606 S INTRON?
L2 2099538 S FOREIGN OR INTRODUC? OR INSERT? OR NON-NATIVE? OR SV40?
L3 4427 S L1 (3N) L2
L4 3384674 S (NUCLEI? ACID) OR SEQUENCE OR (VECTOR (2N) CONTAIN?) OR CDNA
L5 180 S L1 (3N) L2 (3N) L3
L6 178 S L1 (2N) L2 (2N) L3
L7 0 S L6 (2N) POLYMERAS?
L8 85 DUP REM L6 (93 DUPLICATES REMOVED)

```
L9            23 S L8 AND PY<=1995
L10          558 S L1 (3N) L2 (3N) L4
L11          116 S L10 AND POLYMERAS?
L12            0 S L10 (3N) POLYMERAS?
L13           28 S L10 (S) POLYMERAS?
L14           16 DUP REM L13 (12 DUPLICATES REMOVED)
L15            5 S L14 AND PY=<1995
L16            0 S L10 AND (CELL DEATH OR APOPTOS?)
L17           64 S L10 AND (CELL DEATH OR APOPTOS? OR TOXIC? OR KILL? OR INHIB?)
L18           26 S L10 (S) (CELL DEATH OR APOPTOS? OR TOXIC? OR KILL? OR INHIB?)
L19           12 DUP REM L18 (14 DUPLICATES REMOVED)
L20            3 S L19 AND PY=<1995

=> s l10 not Pcr
L21         444 L10 NOT PCR

=> s l21 py<=1995
MISSING OPERATOR L21 PY<=1995
The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> s l21 and py<=1995
   2 FILES SEARCHED...
L22         180 L21 AND PY<=1995

=> dup rem l22
PROCESSING COMPLETED FOR L22
L23           69 DUP REM L22 (111 DUPLICATES REMOVED)

=> d l23 ibib abs 1-10

L23  ANSWER 1 OF 69  CA  COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER:        128:150370  CA
TITLE:                   Construction of plasmid vectors allowing for
                         monitoring of reverse transcriptase and RNase H and
                         their use for detecting inhibitors of retroviral
                         replication
INVENTOR(S):             Garfinkel, David J.; Nissley, Dwight V.; Curcio, Joan
                         M.; Strathern, Jeffrey N.
PATENT ASSIGNEE(S):      United States Dept. of Health and Human Services, USA
SOURCE:                  U.S., 22 pp., Cont.-in-part of U.S. 5,462,873.
                         CODEN: USXXAM
DOCUMENT TYPE:           Patent
LANGUAGE:                English
FAMILY ACC. NUM. COUNT:  2
PATENT INFORMATION:

     PATENT NO.        KIND  DATE          APPLICATION NO.  DATE
     ----------------  ----  --------      ---------------  --------
     US 5714313         A    19980203      US 1995-449207   19950524
     US 5462873         A    19951031      US 1993-102854   19930806 <--
PRIORITY APPLN. INFO.:                   US 1991-668865     19910313
                                         US 1993-102854     19930806
AB   The present invention relates to a DNA segment comprising a selectable
     marker gene, a DNA segment comprising a selectable marker gene inserted
     into a retrotransposon such as the yeast Ty1 element, cells containing these
     DNA segments, and methods of using these DNA segments borne by plasmid
     vectors in host cells.  The present invention further relates to a plasmid
     vector comprising a selectable marker gene inserted into a
     retrotransposon, wherein the retrotransposon comprises a retroviral
     reverse transcriptase/RNase H gene domain and wherein the selectable
     marker gene contains a yeast artificial intron inserted
     into a coding sequence of the marker and the intron is
     in antisense orientation relative to transcription of the marker gene and
```

in sense orientation relative to transcription of the retrotransposon. The reverse transcriptase/RNase H gene domain is derived from retroviruses such as HIV1, HIV2, or avian immunodeficiency, simian immunodeficiency, bovine immunodeficiency, and equine infectious anemia viruses. The constructed vector contains the selectable gene marker HIS3 from yeast and an inducible gene GAL1 promoter.

REFERENCE COUNT: 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L23 ANSWER 2 OF 69 MEDLINE on STN DUPLICATE 1
ACCESSION NUMBER: 96074813 MEDLINE
DOCUMENT NUMBER: PubMed ID: 7476922
TITLE: Inhibition of splicing of wild-type and mutated luciferase-adenovirus pre-mRNAs by antisense oligonucleotides.
AUTHOR: Hodges D; Crooke S T
CORPORATE SOURCE: Department of Anatomy and Neurobiology, University of California, Irvine 92717, USA.
SOURCE: Molecular pharmacology, **(1995 Nov)** 48 (5) 905-18. Journal code: 0035623. ISSN: 0026-895X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199512
ENTRY DATE: Entered STN: 19960124
Last Updated on STN: 19970203
Entered Medline: 19951220

AB We report the construction, characterization, and use of luciferase reporters to test the ability of antisense oligonucleotides to inhibit RNA splicing. beta-Globin and adenovirus **introns** were **inserted** into a luciferase **cDNA**, and luciferase expression was analyzed in transiently transfected cells. The adenovirus reporter expressed large amounts of luciferase, but two beta-globin constructs were inactive. RNA analyses determined that the beta-globin pre-mRNAs were not spliced. Mutagenesis of the beta-globin 5' splice site, branchpoint, and 3' splice site sequences to the adenovirus intron sequences promoted maximal splicing and luciferase activity; reciprocal changes in all three elements of the adenovirus intron eliminated luciferase activity. Wild-type and 3' splice site mutated adenovirus reporters were used to determine the ability of phosphorothioate deoxy and 2' methoxy oligonucleotides to inhibit splicing. RNase H activating oligodeoxynucleotides were better inhibitors of wild-type adenovirus expression than were 2' methoxy analogues. However, 2' methoxy oligonucleotides specific for the branchpoint were more effective inhibitors of splicing of adenovirus transcript containing the beta-globin branchpoint and 3' splice site. We suggest that pre-mRNAs with weak splice sites are potential targets for oligonucleotides that inhibit splicing by occupancy rather than cleavage of the transcripts.

L23 ANSWER 3 OF 69 CA COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 122:288157 CA
TITLE: Splice-mediated insertion of an Alu sequence in the COL4A3 mRNA causing autosomal recessive Alport syndrome
AUTHOR(S): Knebelmann, Bertrand; Forestier, Lionel; Drouot, Laurent; Quinones, Susan; Chuet, Christian; Benessy, France; Saus, Juan; Antignac, Corinne
CORPORATE SOURCE: INSERM, Paris, 75743/15, Fr.
SOURCE: Human Molecular Genetics (**1995**), 4(4), 675-9
CODEN: HMGEE5; ISSN: 0964-6906
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Alport syndrome is mainly an X-linked hereditary disease of basement membranes characterized by progressive renal failure, deafness, and ocular lesions. The α3(IV) and α4(IV) collagen genes have been recently shown to be involved in the less frequent autosomal recessive form. When screening lymphocyte COL4A3 mRNAs from Alport patients, the authors found a mutant whose transcripts were disrupted by a 74 bp insertion at the junction of exons IV or V and VI. The insertion derives from an antisense Alu element in COL4A3 intron V, which has been spliced into that A3(IV) mRNA due to a G to T transversion activating a cryptic acceptor splice site in this Alu element. There is complete segregation of this mutation with the disease in the family. The findings provide the first evidence for the pathogenic role of abnormal splicing of COL4A3. Moreover, the authors demonstrate the superiority of mutation screening at the mRNA level to detect a hitherto poorly recognized mutation mechanism in humans, splice-mediated insertion of an Alu fragment into a coding sequencing.

L23 ANSWER 4 OF 69 MEDLINE on STN DUPLICATE 2
ACCESSION NUMBER: 95222584 MEDLINE
DOCUMENT NUMBER: PubMed ID: 7707369
TITLE: Selection of a remote cleavage site by I-tevI, the td intron-encoded endonuclease.
AUTHOR: Bryk M; Belisle M; Mueller J E; Belfort M
CORPORATE SOURCE: Molecular Genetics Program Wadsworth Center, State University of New York, New York State Department of Health, Albany 12201-0509, USA.
CONTRACT NUMBER: GM-15454 (NIGMS)
GM-39422 (NIGMS)
GM-44844 (NIGMS)
SOURCE: Journal of molecular biology, **(1995 Mar 24)** 247 (2) 197-210.
Journal code: 2985088R. ISSN: 0022-2836.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199505
ENTRY DATE: Entered STN: 19950518
Last Updated on STN: 19950518
Entered Medline: 19950509

AB I-TevI, a double-strand DNA endonuclease involved in the mobility of the td intron of phage T4, is highly unusual in that it binds and cleaves intronless td alleles (td homing sites) in a site-specific but sequence-tolerant manner. The endonuclease binds to **sequences** flanking the **intron insertion** site and near the remote cleavage site, located 23 and 25 nucleotides away on the top and bottom strands, respectively. Mapping studies indicate that I-TevI has both sequence and distance sensors that function during cut-site selection. Although I-TevI cleavage of many insertion and deletion variants of the homing site is impaired, double-strand breaks are generated at positions that collectively span two turns of the helix, indicating that the interaction is extraordinarily flexible. However, the endonuclease does exhibit spacing preferences between its binding domains, and sequence preferences near the cleavage site, with the G:C pair at -23 implicated as a cleavage determinant. Furthermore, I-TevI appears to function through interactions across the minor groove at the cleavage site, as it does at the intron insertion site, and to be capable of cleaving sequentially, first on the bottom and then on the top strand. These properties of I-TevI are incorporated in a model wherein the endonuclease effects distant cleavage via a flexible hinge.

L23 ANSWER 5 OF 69 CA COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 122:98810 CA
TITLE: Isolation, selection and propagation of animal

transgenic stem cells
INVENTOR(S): Smith, Austin Gerard; Mountford, Peter Scott
PATENT ASSIGNEE(S): University of Edinburgh, UK
SOURCE: PCT Int. Appl., 33 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9424274	A1	19941027	WO 1994-GB848	19940421 <--
W: AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, ES, FI, GB, HU, JP, KP, KR, KZ, LK, LU, LV, MG, MN, MW, NL, NO, NZ, PL, PT, RO, RU, SD, SE, SK, UA, US, UZ, VN				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
ZA 9402719	A	19950109	ZA 1994-2719	19940420 <--
ZA 9402720	A	19950330	ZA 1994-2720	19940420 <--
MX 9402851	A	20001031	MX 1994-2851	19940420
CA 2161089	AA	19941027	CA 1994-2161089	19940421 <--
AU 9465426	A1	19941108	AU 1994-65426	19940421 <--
AU 678233	B2	19970522		
EP 695351	A1	19960207	EP 1994-913174	19940421
EP 695351	B1	19991208		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
JP 09500004	T2	19970107	JP 1994-522943	19940421
AT 187491	E	19991215	AT 1994-913174	19940421
IL 109381	A1	20000831	IL 1994-109381	19940421
EP 1403376	A2	20040331	EP 2003-18296	19940421
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE				
US 6146888	A	20001114	US 1995-535141	19951229

PRIORITY APPLN. INFO.:

GB 1993-8271	A	19930421
GB 1993-13323	A	19930628
GB 1994-1011	A	19940120
EP 1994-913175	A3	19940421
WO 1994-GB848	W	19940421

AB Animal stem cells are obtained and maintained by culturing cells containing a selectable marker, whose differential expression enables preferential survival and/or division of the desired stem cells compared to non-stem cells. The selectable marker can be an antibiotic resistance gene. Thus, an engineered neomycin resistance gene (neo), designed to provide an NcoI restriction site at the translation codon, was isolated fro pLZIN as a 1.1-kb XbaI-SphI fragment encompassing encephalomyocarditis virus internal ribosome entry site sequence (EMCV-IRES) and 5'-Neo coding sequences and cloned into pSP72. The KpnI-NcoI EMCV-IRES sequence was replaced with a 1.3-kb Oct4 promoter fragment. Neo3'-coding, rabbit β-globin gene (**intron**) and **SV40** polyadenylation **sequences** were isolated and ligated into the SphI site to generate plasmid Oct4-Neo-βS. An Oct4-Neo-βfos construct incorporated an Oct4-Neo-βS BAMHI fragment 5' to a human c-fos genomic sequence. The Oct4-neo construct (Oct4-tgtvec) was designed for targeted integration into the Oct4 gene. Clonal cells lines of mouse 129 ES cells bearing the 3 plasmid constructs were selected on the basis of their differential survival in medium containing G418 (200 μg/mL) in the presence or absence of DIA. Cultures maintained in DIA-supplemented G418 medium grew as essentially pure ES cells.

L23 ANSWER 6 OF 69 MEDLINE on STN DUPLICATE 3
ACCESSION NUMBER: 94117478 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8288622
TITLE: Structure of the L-histidine decarboxylase gene.
AUTHOR: Yatsunami K; Ohtsu H; Tsuchikawa M; Higuchi T; Ishibashi K;

	Shida A; Shima Y; Nakagawa S; Yamauchi K; Yamamoto M; +
CORPORATE SOURCE:	Japan Tobacco Inc., Pharmaceutical Basic Research Laboratories, Yokohama.
SOURCE:	Journal of biological chemistry, **(1994 Jan 14)** 269 (2) 1554-9. Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY:	United States
DOCUMENT TYPE:	Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:	English
FILE SEGMENT:	Priority Journals
OTHER SOURCE:	GENBANK-D16583
ENTRY MONTH:	199402
ENTRY DATE:	Entered STN: 19940312 Last Updated on STN: 19970203 Entered Medline: 19940222

AB Two species of L-histidine decarboxylase (HDC) mRNA were found in the KU-812-F basophilic cell line, but only the 2.4-kilobase (kb) one encodes the functional HDC (Mamune-Sato, R., Yamauchi, K., Tanno, Y., Ohkawara, Y., Ohtsu, H., Katayose, D., Maeyama, K., Watanabe, T., Shibahara, S., and Takishima, T. (1992) Eur. J. Biochem. 209, 533-539). The 3.4-kb one encodes a truncated HDC protein and is also found in human leukemia-derived cell lines HEL and KCL-22. To clarify the mechanisms that regulate transcription of the HDC gene and generate the two species of mRNA, we have isolated genomic DNA clones coding for the HDC from human genomic libraries. Structural analysis of the isolated clones revealed that the human HDC gene is composed of 12 exons spanning approximately 24 kb. Genomic DNA blot analysis suggested that HDC is encoded by a single copy gene. The structural analysis also demonstrated that the heterogeneity of the HDC mRNA is caused by an **insertion** of the seventh **intron sequence** and alternative use of the splicing acceptor site at the 12th exon. The transcription start site of the HDC gene and the nucleotide sequences of the promoter and first exon regions were determined. We found a TATA-like sequence, a GC box, four CACC boxes, four GATA consensus sequences, and six leader-binding protein-1 binding motifs in the promoter region of the HDC gene.

L23 ANSWER 7 OF 69 CA COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER:	124:222380 CA
TITLE:	Mutator insertions in an intron of the maize knotted1 gene result in dominant suppressible mutations
AUTHOR(S):	Greene, Ben; Walko, Richard; Hake, Sarah
CORPORATE SOURCE:	Plant Gene Expression Center, ARS-USDA, Albany, CA, 94710, USA
SOURCE:	Genetics (**1994**), 138(4), 1275-85 CODEN: GENTAE; ISSN: 0016-6731
PUBLISHER:	Genetics Society of America
DOCUMENT TYPE:	Journal
LANGUAGE:	English

AB The knotted1 (kn1) locus of maize is defined by a series of dominant mutations affecting leaf development. The authors recovered 10 addnl. mutant alleles in lines containing active Mutator transposable elements. Nine of these alleles contain Mu1 or Mu8 elements inserted within a 310-bp region of the kn1 third intron. All five Mu8 insertions are in the same orientation whereas both orientations of Mu1 were recovered. Northern anal. showed that ectopic expression of kn1 within developing leaves is correlated with the mutant phenotype for the four alleles analyzed. Transcript size was not altered. The effect of Mu activity, as measured by the extent of Mu element methylation or by the presence of the autonomous MuDR element, was investigated for two alleles. Kn1-mum2, containing a Mu8 element, and Kn1-mum7, containing a Mu1 element, required Mu activity for the knotted phenotype. The authors examined the effect of Mu activity on ectopic kn1 expression in Kn1-mum2 and found that the transcript was present in leaves of Mu active individuals only. The authors discuss possible mechanisms by which Mu activity could condition

kn1 gene expression.

L23 ANSWER 8 OF 69 MEDLINE on STN DUPLICATE 4
ACCESSION NUMBER: 94258159 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8199591
TITLE: Insertion of a T next to the donor splice site of intron 1 causes aberrantly spliced mRNA in a case of infantile GM1-gangliosidosis.
AUTHOR: Morrone A; Morreau H; Zhou X Y; Zammarchi E; Kleijer W J; Galjaard H; d'Azzo A
CORPORATE SOURCE: Department of Cell Biology and Genetics, Erasmus University, Rotterdam, The Netherlands.
SOURCE: Human mutation, **(1994)** 3 (2) 112-20.
Journal code: 9215429. ISSN: 1059-7794.
PUB. COUNTRY: United States
DOCUMENT TYPE: (CASE REPORTS)
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199407
ENTRY DATE: Entered STN: 19940714
Last Updated on STN: 20000303
Entered Medline: 19940706

AB The lysosomal storage disorders GM1-gangliosidosis and Morquio B syndrome are caused by a complete or partial deficiency of acid beta-galactosidase. Here, we have characterized the mutation segregating in a family with two siblings affected by the severe infantile form of GM1-gangliosidosis. In total mRNA preparations derived from the patients' fibroblasts at least two aberrantly spliced beta-galactosidase transcripts (1 and 2) have been identified. Both transcripts contain a 20 nucleotide (nt) insertion derived from the 5' end of intron 1 of the beta-galactosidase gene. Furthermore, in transcript 2 sequences encoded by exon II are deleted during the splicing process. Comparison of the 20-nt **insertion** with wild-type **intronic sequences** indicated that in the genomic DNA of the patients an extra T nucleotide is present immediately downstream of the conserved GT splice donor dinucleotide of intron 1. Both patients are homozygous for the T nucleotide insertion. We propose that this single base insertion is the mutation responsible for aberrant splicing of beta-galactosidase pre-mRNA, giving rise to transcripts that cannot encode a normal protein.

L23 ANSWER 9 OF 69 MEDLINE on STN DUPLICATE 5
ACCESSION NUMBER: 93252823 MEDLINE
DOCUMENT NUMBER: PubMed ID: 8387498
TITLE: High-level and erythroid-specific expression of human glucose-6-phosphate dehydrogenase in transgenic mice.
AUTHOR: Tang T K; Tam K B; Huang S C
CORPORATE SOURCE: Institute of Biomedical Sciences, Academia Sinica, Taipei, Taiwan, Republic of China.
SOURCE: Journal of biological chemistry, **(1993 May 5)** 268 (13) 9522-5.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199306
ENTRY DATE: Entered STN: 19930618
Last Updated on STN: 19970203
Entered Medline: 19930604

AB Human Glc-6-P dehydrogenase (Glc-6-P) cDNA spanning the entire coding region was subcloned into a pSG5 **vector** that **contains** an early **SV40** promoter, **intron** II of the rabbit beta-globin gene, and a polyadenylation signal. This expression cassette

was then placed downstream of the human beta-globin locus control region and injected into fertilized mouse eggs. Among five transgenic founders that contained intact copies of the construct, one founder expressed human Glc-6-P dehydrogenase enzyme in a high-level and erythroid-specific fashion (5 x higher than endogenous Glc-6-P dehydrogenase activity). When this male founder mated with a normal individual, all the offspring that carried the transgene showed high-level expression of Glc-6-P dehydrogenase activity in erythroid cells. The endogenous mouse Glc-6-P dehydrogenase in all high-expression mice could be competed out by forming a hybrid with human Glc-6-P dehydrogenase. Our results indicate that the locus control region can drive the human Glc-6-P dehydrogenase gene to be specifically expressed in the erythroid cells of transgenic mice. The results described here provide a basis for experiments designed to express human Glc-6-P dehydrogenase in transgenic mice and suggest a suitable approach to producing a mouse model for studying human Glc-6-P dehydrogenase deficiency.

L23 ANSWER 10 OF 69 CA COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 120:97641 CA
TITLE: Nucleotide sequence of a Chlorella vulgaris α-tubulin gene
AUTHOR(S): Yamada, Takashi; Maki, Shinya; Higashiyama, Takanobu
CORPORATE SOURCE: Fac. Eng., Hiroshima Univ., Higashi-Hiroshima, 724, Japan
SOURCE: Plant Physiology (**1993**), 103(4), 1467
CODEN: PLPHAY; ISSN: 0032-0889
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The authors report the nucleotide and deduced amino acid sequences of a genomic clone (MAK555) encoding the α-tubulin from C. vulgaris (IAM C-169). The gene contained 9 introns; the number, length, **sequence** and **insertion** position of the **introns** were significantly different from those of two other green algae, Chlamydomonas reinhardtii and Volvox carteri. However, the first intron is inserted at the same site of the gene among the 3 green algae. Two putative regulatory elements, similar to those reported for Chlamydomonas genes were found at positions 78-96 and 191-206. The codon usage in the Chlorella α-tubulin gene is strongly biased; in general, C or G residues at the third position of codons are preferred (87.3%) and NNA codons are rarely used (2.7%).

=> d his

(FILE 'HOME' ENTERED AT 16:49:57 ON 06 JUL 2004)

FILE 'MEDLINE, BIOSIS, EMBASE, CA, SCISEARCH' ENTERED AT 16:50:07 ON 06 JUL 2004

L1 147606 S INTRON?
L2 2099538 S FOREIGN OR INTRODUC? OR INSERT? OR NON-NATIVE? OR SV40?
L3 4427 S L1 (3N) L2
L4 3384674 S (NUCLEI? ACID) OR SEQUENCE OR (VECTOR (2N) CONTAIN?) OR CDNA
L5 180 S L1 (3N) L2 (3N) L3
L6 178 S L1 (2N) L2 (2N) L3
L7 0 S L6 (2N) POLYMERAS?
L8 85 DUP REM L6 (93 DUPLICATES REMOVED)
L9 23 S L8 AND PY<=1995
L10 558 S L1 (3N) L2 (3N) L4
L11 116 S L10 AND POLYMERAS?
L12 0 S L10 (3N) POLYMERAS?
L13 28 S L10 (S) POLYMERAS?
L14 16 DUP REM L13 (12 DUPLICATES REMOVED)
L15 5 S L14 AND PY=<1995
L16 0 S L10 AND (CELL DEATH OR APOPTOS?)

```
L17          64 S L10 AND (CELL DEATH OR APOPTOS? OR TOXIC? OR KILL? OR INHIB?)
L18          26 S L10 (S) (CELL DEATH OR APOPTOS? OR TOXIC? OR KILL? OR INHIB?)
L19          12 DUP REM L18 (14 DUPLICATES REMOVED)
L20           3 S L19 AND PY=<1995
L21         444 S L10 NOT PCR
L22         180 S L21 AND PY<=1995
L23          69 DUP REM L22 (111 DUPLICATES REMOVED)

=> s l23 and (bacteri? or pro!aryot? or viral or virus or virio?)
L24         26 L23 AND (BACTERI? OR PRO!ARYOT? OR VIRAL OR VIRUS OR VIRIO?)

=> s l23 and ((bacteri? or pro!aryot? or viral or virus or virio?) (s) l4)
   4 FILES SEARCHED...
L25         17 L23 AND ((BACTERI? OR PRO!ARYOT? OR VIRAL OR VIRUS OR VIRIO?)
               (S) L4)

=> d l25 1-17 ibib abs

L25  ANSWER 1 OF 17     MEDLINE on STN
ACCESSION NUMBER:   92375687     MEDLINE
DOCUMENT NUMBER:    PubMed ID: 1508686
TITLE:              Intron 1 and the 5'-flanking region of the human
                    thymidylate synthase gene as a regulatory determinant of
                    growth-dependent expression.
AUTHOR:             Takayanagi A; Kaneda S; Ayusawa D; Seno T
CORPORATE SOURCE:   Laboratory of Mutagenesis, Graduate University for Advanced
                    Studies, Mishima, Japan.
SOURCE:             Nucleic acids research, (1992 Aug 11) 20 (15)
                    4021-5.
                    Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY:       ENGLAND: United Kingdom
DOCUMENT TYPE:      Journal; Article; (JOURNAL ARTICLE)
LANGUAGE:           English
FILE SEGMENT:       Priority Journals
ENTRY MONTH:        199209
ENTRY DATE:         Entered STN: 19921009
                    Last Updated on STN: 19980206
                    Entered Medline: 19920923
AB   We have determined the regulatory regions responsible for the
     growth-dependent expression of the human thymidylate synthase (TS) gene,
     using a set of minigenes constructed from segments of the human TS gene
     and the cDNA clone.  Each construct was introduced stably into a
     TS-negative mutant of rat fibroblast 3Y1 cells.  By serum-restricted
     synchronization of the cloned transformant cells, we found that a minigene
     with the genomic 5'-flanking region and intron 1 without other introns
     were sufficient for the normal extent and pattern of S-phase specific
     expression at the levels of both mRNA and enzymatic activity.  In
     contrast, a TS cDNA clone driven by an SV40-based expression vector showed
     constitutive expression.  Insertion of intron 1 into
     the cDNA clone in the normal location, or replacement of the
     viral 5'-promoter region of the cDNA clone by the
     genomic 5'-flanking sequence converted the constitutive
     expression to the S-phase dependent one, but only partly, that is,
     coexistence of the two regions were required for the normal expression.
     Results obtained by nuclear run-on assay suggested that
     posttranscriptional controls are also involved in this regulation in
     consistent with our previous results with the bona fide human TS gene.

L25  ANSWER 2 OF 17     MEDLINE on STN
ACCESSION NUMBER:   92353391     MEDLINE
DOCUMENT NUMBER:    PubMed ID: 1322741
TITLE:              Expression in transgenic tobacco of the bacterial neomycin
                    phosphotransferase gene modified by intron insertions of
                    various sizes.
```

AUTHOR: Paszkowski J; Peterhans A; Bilang R; Filipowicz W
CORPORATE SOURCE: Swiss Federal Institute of Technology, Institute of Plant Sciences, ETH-Zentrum, Zurich.
SOURCE: Plant molecular biology, **(1992 Aug)** 19 (5) 825-36.
Journal code: 9106343. ISSN: 0167-4412.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199209
ENTRY DATE: Entered STN: 19920925
Last Updated on STN: 19980206
Entered Medline: 19920908

AB A plant selectable marker gene consisting of cauliflower mosaic **virus** expression signals and the protein-**coding sequence** of **bacterial** neomycin phosphotransferase was modified by **insertion** of an **intron sequence** from a storage protein gene, phaseolin. Correct and efficient splicing of the resulting mosaic RNA was observed in transgenic tobacco plants. The insertion of various linkers or gradual increase of intron size by addition in both orientations of internal intron sequences from another plant gene (parsley, 4-coumarate ligase) had little or no effect on the precision of slicing. The gene activity measured by selectability assay in the protoplast transformation showed that only introns enlarged to 1161 bases and longer caused decreased selectability. The suitability of such mosaic marker genes for studies of RNA splicing, DNA recombination and early events after infection of plants with Agrobacterium is discussed.

L25 ANSWER 3 OF 17 MEDLINE on STN
ACCESSION NUMBER: 91279455 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2057358
TITLE: In vivo analysis of plant pre-mRNA splicing using an autonomously replicating vector.
AUTHOR: McCullough A J; Lou H; Schuler M A
CORPORATE SOURCE: Department of Plant Biology, University of Illinois, Urbana 61801.
CONTRACT NUMBER: GM39025 RO1 (NIGMS)
SOURCE: Nucleic acids research, **(1991 Jun 11)** 19 (11) 3001-9.
Journal code: 0411011. ISSN: 0305-1048.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199107
ENTRY DATE: Entered STN: 19910818
Last Updated on STN: 19910818
Entered Medline: 19910731

AB In this paper, we demonstrate that an autonomously replicating plant expression vector can be used for analysis of pre-mRNA splicing determinants in intact dicot cells. This vector system relies on the Agrobacterium-mediated transfection of leaf discs with the A component of the geminivirus tomato golden mosaic virus (TGMV). **Insertion** of **intron sequences** between **viral** promoter and terminator **sequences** results in the production of high levels of pre-mRNA transcripts that are effectively and accurately spliced in vivo. Introns from the soybean B-conglycinin gene are spliced at greater than 95% efficiency indicating that the high expression levels of precursor RNA do not exceed the intron splicing capacity of these cells. Introns from the pea and wheat rbcS genes are spliced at 85% and 73% efficiency, respectively, indicating that tobacco leaf disc nuclei are capable of effectively and accurately processing particular dicot and monocot introns. Inclusion of a dicot intron in an engineered construct results

in a five-fold enhancement of the level of mRNA stably expressed in dicot nuclei.

L25 ANSWER 4 OF 17 MEDLINE on STN
ACCESSION NUMBER: 91248464 MEDLINE
DOCUMENT NUMBER: PubMed ID: 1370034
TITLE: Comparison of human lymphotoxin gene expression in CHO cells directed by genomic DNA or cDNA sequences.
AUTHOR: Yamashita K; Ikenaka Y; Kakutani T; Kawaharada H; Watanabe K
CORPORATE SOURCE: Biochemical Research Laboratories, Kanegafuchi Chemical Industry Co., Ltd., Hyogo, Japan.
SOURCE: Agricultural and biological chemistry, **(1990 Nov)** 54 (11) 2801-9.
Journal code: 0370452. ISSN: 0002-1369.
PUB. COUNTRY: Japan
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Biotechnology
ENTRY MONTH: 199107
ENTRY DATE: Entered STN: 19950809
Last Updated on STN: 19960129
Entered Medline: 19910708

AB Four recombinant plasmids coding for human lymphotoxin (LT) were constructed with genomic DNA (gDNA) or cDNA sequences. The simian **virus** 40 (SV40) early region, which contains the early promoter, an intron of the small-t-antigen-encoding gene, and polyadenylation signal **sequences**, was used for transcriptional and post-transcriptional regulatory elements in the construction of these plasmids. Two of them contained gDNA and the other two contained cDNA. One of the gDNA plasmids and one of the **cDNA** plasmids carry the **SV40 intron** between the structural gene and polyadenylation signal. Transient and stable gene expression levels of these plasmids in Chinese hamster ovary (CHO) cells were measured by assaying the secreted LT. The plasmid carrying gDNA without the SV40 intron was expressed more efficiently than the other three plasmids in both transient and stable gene expression assays.

L25 ANSWER 5 OF 17 MEDLINE on STN
ACCESSION NUMBER: 89039878 MEDLINE
DOCUMENT NUMBER: PubMed ID: 3185558
TITLE: Short donor site **sequences inserted** within the **intron** of beta-globin pre-mRNA serve for splicing in vitro.
AUTHOR: Mayeda A; Ohshima Y
CORPORATE SOURCE: Graduate School of Medical Sciences, University of Tsukuba, Ibaraki, Japan.
SOURCE: Molecular and cellular biology, **(1988 Oct)** 8 (10) 4484-91.
Journal code: 8109087. ISSN: 0270-7306.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198812
ENTRY DATE: Entered STN: 19900308
Last Updated on STN: 19970203
Entered Medline: 19881221

AB We constructed SP6-human beta-globin derivative plasmids that included possible donor site (5' splice site) sequences at a specified position within the first intron. The runoff transcripts from these templates truncated in the second exon were examined for splicing in a nuclear extract from HeLa cells. In addition to the products from the authentic donor site, a corresponding set of novel products from the inserted,

alternative donor site was generated. Thus, a short **sequence inserted** within an **intron** can be an active donor site signal in the presence of an authentic donor site. The active donor site **sequences** included a 9-nucleotide consensus **sequence**, 14- or 16-nucleotide **sequences** at the human beta-globin first or second donor, and those at simian **virus** 40 large T antigen or small t antigen donor. These included 3 to 8 nucleotides of an exon and 6 to 8 nucleotides of an intron. The activity of the inserted donor site relative to that of the authentic donor site depended on the donor sequence inserted. The relative activity also strongly depended on the concentrations of both KCl (40 to 100 mM) and MgCl2 (1.6 to 6.4 mM). At the higher KCl concentrations tested, all the inserted, or proximate, donor sites were more efficiently used. Under several conditions, some inserted donor sites were more active than was the authentic donor site. Our system provides an in vitro assay for donor site activity of a sequence to be tested.

L25 ANSWER 6 OF 17 MEDLINE on STN
ACCESSION NUMBER: 88054470 MEDLINE
DOCUMENT NUMBER: PubMed ID: 2824147
TITLE: Expression of human uterine tissue-type plasminogen activator in mouse cells using BPV vectors.
AUTHOR: Reddy V B; Garramone A J; Sasak H; Wei C M; Watkins P; Galli J; Hsiung N
CORPORATE SOURCE: Integrated Genetics, 31 New York Avenue, Framingham, MA 01701.
SOURCE: DNA (Mary Ann Liebert, Inc.), **(1987 Oct)** 6 (5) 461-72.
Journal code: 8302432. ISSN: 0198-0238.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M18182
ENTRY MONTH: 198801
ENTRY DATE: Entered STN: 19900305
Last Updated on STN: 19980206
Entered Medline: 19880114

AB Human tissue-type plasminogen activator (t-PA) cDNA was cloned from uterine tissue and engineered in expression vectors for production in mouse C127 cells. The vectors consisted of the bovine papilloma **virus**-1 (BPV-1) genome and t-PA transcriptional unit with a mouse metallothionein (MT-1) promoter at the 5' end and MT-1 genomic **sequences** or **SV40** early **introns** and polyadenylation signals at the 3' end. Analysis of the expression vectors transfected into cells revealed that t-PA is expressed 100- to 200-fold more with an intronless vector utilizing the SV40 polyadenylation signal than with other, intron-containing vectors. RNA analysis of stable cell lines indicated that t-PA expression levels correlated with mRNA abundance. DNA copy number and transcriptional rate of the MT-1 promoter remained constant in cell lines transformed by different BPV expression vectors. Uterine t-PA produced by recombinant DNA means was enzymatically active and similar in properties to Bowes melanoma t-PA.

L25 ANSWER 7 OF 17 MEDLINE on STN
ACCESSION NUMBER: 87064569 MEDLINE
DOCUMENT NUMBER: PubMed ID: 3023944
TITLE: Downstream sequences affect transcription initiation from the adenovirus major late promoter.
AUTHOR: Mansour S L; Grodzicker T; Tjian R
SOURCE: Molecular and cellular biology, **(1986 Jul)** 6 (7) 2684-94.
Journal code: 8109087. ISSN: 0270-7306.
PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198701
ENTRY DATE: Entered STN: 19900302
Last Updated on STN: 19900302
Entered Medline: 19870120

AB We analyzed a set of adenovirus-simian **virus** 40 (SV40) hybrids in which the SV40 T antigen **coding sequences** are inserted downstream from the adenovirus major late promoter within the first, second, and third segments of the tripartite leader. In infected cells, these viruses give rise to a matched set of hybrid SV40 mRNAs that differ only in the number of tripartite leader segments attached to the complete SV40 T antigen coding region. We found that the number of tripartite leader segments present at the 5' end of the hybrid SV40 mRNAs had little effect on the efficiency of T antigen translation. Surprisingly, insertion of SV40 sequences within the first leader segment, at +33 relative to the start of transcription, significantly reduced the frequency of transcription initiation from the major late promoter. The 3' boundary of this downstream transcriptional control element was mapped between +33 and +190 by showing that insertion of **SV40 sequences** within the **intron** after the first leader segment at +190 had very little effect on transcription initiation from the late promoter. A transient expression assay was used to show that the effect of downstream sequences on transcription initiation from the major late promoter is dependent on a trans-acting factor encoded or induced by adenovirus.

L25 ANSWER 8 OF 17 MEDLINE on STN
ACCESSION NUMBER: 85134874 MEDLINE
DOCUMENT NUMBER: PubMed ID: 6098686
TITLE: Efficient expression of cloned complementary DNAs for secretory proteins after injection into Xenopus oocytes.
AUTHOR: Krieg P; Strachan R; Wallis E; Tabe L; Colman A
SOURCE: Journal of molecular biology, **(1984 Dec 15)** 180 (3) 615-43.
Journal code: 2985088R. ISSN: 0022-2836.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198504
ENTRY DATE: Entered STN: 19900320
Last Updated on STN: 19900320
Entered Medline: 19850404

AB Cloned complementary DNAs encoding chicken ovalbumin, chicken prelysozyme and calf preprochymosin, prochymosin and chymosin were inserted downstream from various viral promoters in modified recombinant "shuttle" vectors. Microinjection of the ovalbumin, prelysozyme and preprochymosin constructs into the nuclei of Xenopus laevis oocytes resulted in the synthesis, segregation in membranes and secretion into the extracellular medium of ovalbumin, lysozyme and prochymosin, respectively. Judging from molecular weight estimations, lysozyme and prochymosin were correctly proteolytically processed while ovalbumin, which lacks a cleavable signal sequence, was glycosylated. Injection of the DNA construct encoding prochymosin without its signal sequence resulted in synthesis of prochymosin protein that was localized exclusively in the oocyte cytoplasm. No immunospecific protein was detected after injection of the DNA encoding mature chymosin. In terms of protein expression in oocytes, the Herpes simplex thymidine kinase (TK) promoter was up to sevenfold more effective than the simian virus 40 (SV40) early promoter, and equally as effective as the Moloney murine sarcoma virus long terminal repeat element. Where tested, protein expression in oocytes was much reduced if DNA **sequences** encoding the **SV40** small t **intron**

and its flanking **sequences** were present in the constructs. S1 nuclease mapping of transcripts produced after injection of DNAs containing the TK promoter indicated that the majority of transcripts initiated at, or within, two bases of the known "cap" site. However, minor transcripts initiating upstream from this site were observed and one (or more) of these transcripts was responsible for the synthesis of an ovalbumin polypeptide containing a 51 amino acid N-terminal extension. This extended protein remained in the oocyte cytosol. When ovalbumin **cDNA** was inserted into the vectors with opposite polarity to the **viral** promoter, expression in oocytes resulted in the predominant synthesis and secretion of a variant ovalbumin with a 21 amino acid N-terminal extension, although some full-length ovalbumin was also synthesized and secreted. S1 mapping revealed the presence, in these oocytes, of transcripts of predicted polarity initiating 118 bases upstream from the wild type ovalbumin initiator ATG, at a previously unreported SV40 "promoter". No protein synthesis was detected after the injection of these reverse-orientation constructs into baby hamster kidney (BHK-21) cells.

L25 ANSWER 9 OF 17 MEDLINE on STN
ACCESSION NUMBER: 81223699 MEDLINE
DOCUMENT NUMBER: PubMed ID: 6264427
TITLE: Expression of simian virus 40-rat preproinsulin recombinants in monkey kidney cells: use of preproinsulin RNA processing signals.
AUTHOR: Gruss P; Khoury G
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, **(1981 Jan)** 78 (1) 133-7.
Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198108
ENTRY DATE: Entered STN: 19900316
Last Updated on STN: 19900316
Entered Medline: 19810820

AB The complete rat preproinsulin gene I was cloned into a simian virus 30 (SV 40) vector. Most of the late region of the **viral** vector, including the **SV40** intervening **sequences** (**introns**) and all of the major splice junctions, was deleted and replaced by the entire rat insulin gene. The recombinant molecules and a temperature-sensitive helper virus (tsA28) were inoculated into monkey kidney cultures. The formation of stable transcripts of the insulin insert was as efficient as the production of late SV40 mRNA. Analysis of these transcripts indicated that the rat preproinsulin gene nucleotide signals involved in RNA splicing and poly(A) addition were used. Examination of the 5' ends of the mRNAs showed several classes, one of which was the same size as the authentic rat insulinoma mRNA. This suggests that a portion of the transcripts may be initiated or processed faithfully, or both, at their 5' ends within rat insulin sequences. Significant quantities of a protein identified as rat proinsulin were synthesized. Detection of most of the proinsulin in the tissue culture medium suggests that this protein was secreted.

L25 ANSWER 10 OF 17 EMBASE
on STN
ACCESSION NUMBER: 89009828 EMBASE
DOCUMENT NUMBER: 1989009828
TITLE: New BK virus episomal vector for complementary DNA expression in human cells.
AUTHOR: Grossi M.P.; Caputo A.; Rimessi P.; Chiccolli L.; Balboni P.G.; Barbanti-Brodano G.

CORPORATE SOURCE: Institute of Microbiology, School of Medicine, University of Ferrara, 44100 Ferrara, Italy
SOURCE: Archives of Virology, (1988) 102/3-4 (275-283).
ISSN: 0304-8608 CODEN: ARVIDF
COUNTRY: Austria
DOCUMENT TYPE: Journal
FILE SEGMENT: 004 Microbiology
022 Human Genetics
047 Virology
LANGUAGE: English
SUMMARY LANGUAGE: English

AB The properties of pRP-c, a new vector for complementary DNA (**cDNA**) expression, are described. The **vector contains** the early region and replication origin of BK **virus** (BKV), a human papovavirus. Due to the presence of these BKV **sequences**, pRP-c replicates in human cells allowing amplification of **inserted cDNAs.** The promoter, **intron** and polyadenylation region for **cDNA** expression are separated by unique restriction sites and can therefore be individually excised and substituted with different transcription signals. **Coding sequences** of the **bacterial** genes for chloramphenicol-acetyl transferase (CAT) or neomycin phosphotransferase (neo) were inserted into the **cDNA** cloning site of pRP-c and expressed in human cells in transient assays or stable clones. In both cases expression of the inserted **sequences** was significantly more efficient than by using the integration vectors pSV2CAT and pSV2neo, demonstrating the advantages of episomal expression vectors in human cells. Possible uses of pRP-c to express **viral** and cellular **cDNAs** in human cells are discussed.

L25 ANSWER 11 OF 17 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED. on STN
ACCESSION NUMBER: 86006599 EMBASE
DOCUMENT NUMBER: 1986006599
TITLE: Inactivation of p53 gene expression by an insertion of Moloney murine leukemia **virus**-like DNA **sequences.**
AUTHOR: Wolf D.; Rotter V.
CORPORATE SOURCE: Department of Cell Biology, The Weizmann Institute of Science, Rehovot 76100, Israel
SOURCE: Molecular and Cellular Biology, (1984) 4/7 (1402-1410).
CODEN: MCEBD4
COUNTRY: United States
DOCUMENT TYPE: Journal
FILE SEGMENT: 047 Virology
022 Human Genetics
016 Cancer
LANGUAGE: English

AB Analysis of Abelson murine leukemia **virus**-transformed L12 cells which lack the p53 cellular encoded tumor antigen revealed alterations in the p53-specific genomic DNA **sequences.** The active p53 gene, usually contained in a 16-kilobase EcoRI DNA fragment of p53 producer cells, went through major alterations leading to the appearance of a substantially larger 28.0-kilobase p53-specific EcoRI fragment. Detailed restriction enzyme analysis, with genomic probes spanning throughout the whole active p53 gene, indicated that the L12 p53 altered gene contains all the exons and principal introns of the normal p53 16.0-kilobase gene. However, its structure was interrupted by the integration of a novel DNA segment into the noncoding intervening **sequences** of the first p53 **intron.** Analysis of the **inserted sequences** revealed close homology to Moloney murine leukemia **virus.** This Moloney leukemia murine **virus**-like particle resides in a 5' to 3' transcriptional orientation, similar to the p53 gene, permitting the transcription of aberrant fused mRNA molecules detected in these cells.

L25 ANSWER 12 OF 17 CA COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 122:98810 CA
TITLE: Isolation, selection and propagation of animal transgenic stem cells
INVENTOR(S): Smith, Austin Gerard; Mountford, Peter Scott
PATENT ASSIGNEE(S): University of Edinburgh, UK
SOURCE: PCT Int. Appl., 33 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9424274	A1	19941027	WO 1994-GB848	19940421 <--
W: AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, ES, FI, GB, HU, JP, KP, KR, KZ, LK, LU, LV, MG, MN, MW, NL, NO, NZ, PL, PT, RO, RU, SD, SE, SK, UA, US, UZ, VN				
RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
ZA 9402719	A	19950109	ZA 1994-2719	19940420 <--
ZA 9402720	A	19950330	ZA 1994-2720	19940420 <--
MX 9402851	A	20001031	MX 1994-2851	19940420
CA 2161089	AA	19941027	CA 1994-2161089	19940421 <--
AU 9465426	A1	19941108	AU 1994-65426	19940421 <--
AU 678233	B2	19970522		
EP 695351	A1	19960207	EP 1994-913174	19940421
EP 695351	B1	19991208		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE				
JP 09500004	T2	19970107	JP 1994-522943	19940421
AT 187491	E	19991215	AT 1994-913174	19940421
IL 109381	A1	20000831	IL 1994-109381	19940421
EP 1403376	A2	20040331	EP 2003-18296	19940421
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE				
US 6146888	A	20001114	US 1995-535141	19951229

PRIORITY APPLN. INFO.:

GB 1993-8271	A	19930421
GB 1993-13323	A	19930628
GB 1994-1011	A	19940120
EP 1994-913175	A3	19940421
WO 1994-GB848	W	19940421

AB Animal stem cells are obtained and maintained by culturing cells containing a selectable marker, whose differential expression enables preferential survival and/or division of the desired stem cells compared to non-stem cells. The selectable marker can be an antibiotic resistance gene. Thus, an engineered neomycin resistance gene (neo), designed to provide an NcoI restriction site at the translation codon, was isolated fro pLZIN as a 1.1-kb XbaI-SphI fragment encompassing encephalomyocarditis **virus** internal ribosome entry site **sequence** (EMCV-IRES) and 5'-Neo **coding sequences** and cloned into pSP72. The KpnI-NcoI EMCV-IRES sequence was replaced with a 1.3-kb Oct4 promoter fragment. Neo3'-coding, rabbit β-globin gene (**intron**) and **SV40** polyadenylation **sequences** were isolated and ligated into the SphI site to generate plasmid Oct4-Neo-βS. An Oct4-Neo-βfos construct incorporated an Oct4-Neo-βS BAMHI fragment 5' to a human c-fos genomic sequence. The Oct4-neo construct (Oct4-tgtvec) was designed for targeted integration into the Oct4 gene. Clonal cells lines of mouse 129 ES cells bearing the 3 plasmid constructs were selected on the basis of their differential survival in medium containing G418 (200 μg/mL) in the presence or absence of DIA. Cultures maintained in DIA-supplemented G418 medium grew as essentially pure ES cells.

L25 ANSWER 13 OF 17 CA COPYRIGHT 2004 ACS on STN

ACCESSION NUMBER: 116:35640 CA
TITLE: New diagnostic and treatment methods involving the cystic fibrosis transmembrane regulator
INVENTOR(S): Gregory, Richard J.; Cheng, Seng H.; Smith, Alan; Paul, Sucharita; Hehir, Kathleen M.; Marshall, John
PATENT ASSIGNEE(S): Genzyme Corp., USA
SOURCE: Eur. Pat. Appl., 49 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 7
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 446017	A1	19910911	EP 1991-301819	19910305 <--
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE				
CA 2037478	AA	19910906	CA 1991-2037478	19910304 <--
JP 06303978	A2	19941101	JP 1991-38810	19910305 <--
US 5981714	A	19991109	US 1996-691605	19960815
US 5750571	A	19980512	US 1996-774127	19961223
US 2002164782	A1	20021107	US 2000-568756	20000511
AU 765709	B2	20030925	AU 2000-53512	20000821
US 2003147854	A1	20030807	US 2002-161539	20020603

PRIORITY APPLN. INFO.:

US 1990-488307	A	19900305
US 1990-589295	A	19900927
US 1990-613592	A	19901115
US 1992-935603	B2	19920826
US 1992-985478	B2	19921203
US 1993-72708	A1	19930607
US 1993-87132	A2	19930702
AU 1997-43655	A3	19971031
US 1998-114950	B1	19980827
US 1999-248026	A1	19990210
US 2000-568756	B1	20000511

AB A cDNA for the complete human cystic fibrosis transmembrane conductance regulator (CFTCR) is provided. A method for stabilizing CFTER clones comprises placing it in a low-copy number plasmid, **inserting** an **intron** into the **coding sequence**, and/or altering the sequence to remove cryptic RNA polymerase promoter sequences. The CFTCR cDNA can be used to produce the CFTCR, to treat cystic fibrosis, to prepare transgenic animals, and to diagnose CFTCR dysfunction. Many mutations known to occur in cystic fibrosis patients were introduced into CFTCR cDNA, and this mutant cDNA was expressed in COS-7 cells. The mutations Δ phenylalanine-508, Δ isoleucine-507, lysine-464 changes to methionine, phenylalanine-508 changed to arginine, and serine-549 changed to isoleucine resulted in production of unstable, incompletely glycosylated CFTCR.

L25 ANSWER 14 OF 17 CA
ACCESSION NUMBER: 115:224978 CA
TITLE: I-TevI, the endonuclease encoded by the mobile td intron, recognizes binding and cleavage domains on its DNA target
AUTHOR(S): Bell-Pedersen, Deborah; Quirk, Susan M.; Bryk, Mary; Belfort, Marlene
CORPORATE SOURCE: Wadsworth Cent. Lab. Res., New York State Dep. Health, Albany, NY, 12201-0509, USA
SOURCE: Proceedings of the National Academy of Sciences of the United States of America (**1991**), 88(17), 7719-23
CODEN: PNASA6; ISSN: 0027-8424
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Mobility of the phage T4 td intron depends on activity of an intron-encoded endonuclease (I-TevI), which cleaves a homologous intronless (ΔIn) target gene. The double-strand break initiates a recombination event that leads to intron transfer. It was found previously that I-TevI cleaves tdΔIn target DNA 23-26 nucleotides upstream of the intron insertion site. DNase I-footprinting expts. and gel-shift assays indicate that I-TevI makes primary contacts around the intron insertion site. A synthetic DNA duplex spanning the insertion site but lacking the cleavage site was shown to bind I-TevI specifically, and when cloned, to direct cleavage into vector sequences. The behavior of the cloned duplex and that of deletion and insertion mutants support a primary role for sequences surrounding the insertion site in directing I-TevI binding, conferring cleavage ability, and determining cleavage polarity. On the other hand, sequences around the cleavage site were shown to influence cleavage efficiency and cut-site selection. The role of cleavage-site sequences in determining cleavage distance argues against a strict "ruler" mechanism for cleavage by I-TevI. The complex nature of the homing site recognized by this unusual type of endonuclease is considered in the context of intron spread.

L25 ANSWER 15 OF 17 CA COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 108:1566 CA
TITLE: Eukaryotic cDNA containing intron(s) for enhanced expression
INVENTOR(S): Schumacher, Guenter; Hirth, Peter; Buckel, Peter
PATENT ASSIGNEE(S): Boehringer Mannheim G.m.b.H., Fed. Rep. Ger.
SOURCE: Ger. Offen., 8 pp.
CODEN: GWXXBX
DOCUMENT TYPE: Patent
LANGUAGE: German
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
DE 3545126	A1	19870625	DE 1985-3545126	19851219 <--
ZA 8609487	A	19870930	ZA 1986-9487	19861218 <--
EP 227064	A1	19870701	EP 1986-117750	19861219 <--
R: ES, GR				
WO 8703904	A1	19870702	WO 1986-EP763	19861219 <--
W: AU, DK, FI, JP, KR, US				
RW: AT, BE, CH, DE, FR, GB, IT, LU, NL, SE				
AU 8768333	A1	19870715	AU 1987-68333	19861219 <--
AU 600253	B2	19900809		
JP 62502942	T2	19871126	JP 1987-500485	19861219 <--
EP 250513	A1	19880107	EP 1987-900133	19861219 <--
EP 250513	B1	19910911		
R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE				
DD 263079	A5	19881221	DD 1986-298023	19861219 <--
AT 67242	E	19910915	AT 1987-900133	19861219 <--
ES 2026206	T3	19920416	ES 1987-900133	19861219 <--
FI 8703572	A	19870818	FI 1987-3572	19870818 <--
DK 8704329	A	19870819	DK 1987-4329	19870819 <--

PRIORITY APPLN. INFO.:

DE 1985-3545126	19851219
EP 1987-900133	19861219
WO 1986-EP763	19861219

AB Eukaryotic gene expression can be increased if an **intron** is **inserted** into the **cDNA** and the resulting gene is cloned in **prokaryotes** before being transferred to an eukaryotic cell for expression. A plasmid (pBT 94) containing the complete tissue plasminogen activator (tPA) cDNA into which the naturally occurring intron C has been inserted (at the position corresponding to its position in the gene) was constructed. This tPA-encoding DNA was then inserted into another plasmid

containing SV40- and pBR322-derived **sequences** to prepare pBT 102, which was amplified in a **prokaryote.** Plasmid pBT 102-transfected CV-1 cells produced .apprx.2-fold more tPA relative to the same cells containing a plasmid in which the gene did not contain the intron.

L25 ANSWER 16 OF 17 CA COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 101:223834 CA
TITLE: Modification of p53 gene expression by integration of a foreign DNA element
AUTHOR(S): Wolf, D.; Rotter, V.
CORPORATE SOURCE: Dep. Cell Biol., Weizmann Inst. Sci., Rehovot, Israel
SOURCE: Cancer Cells (1984-1989) (**1984**), 2(Oncog. Viral Genes), 403-9
CODEN: CACEEG; ISSN: 0743-2194
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A 13.5-kilobase (kb) DNA insert unique to the Abelson murine leukemia virus (Ab-MLV)-transformed mouse lymphoid cell line L12 was integrated in the active p53 tumor antigen gene. The inability of L12 cells to produce P53 was due to the absence of mature 2.0-kb p53-specifying mRNA. Instead, 2 major p53-specific species of 3.5 and 6.5 kb were present. Apparently the L12 p53 gene contains all the exons and principal introns of the normal 16-kb p53 gene, and its function is interrupted by the DNA sequence insert in the noncoding intervening sequence. Anal. of the DNA insert showed homol. with Molney murine leukemia virus (Mo-MLV). Perhaps, the initial step of establishing the L12 cell line involved the infection of bone marrow cells with a stock containing Ab-MLV and Mo-MLV and included a genetic event where the Mo-MLV-specific **sequence** was **inserted** into the 1st **intron** of the p53 gene.

L25 ANSWER 17 OF 17 CA COPYRIGHT 2004 ACS on STN
ACCESSION NUMBER: 97:50599 CA
TITLE: The expression of the influenza virus hemagglutinin gene from SV40-HA recombinants
AUTHOR(S): Gething, Mary Jane; Sambrook, Joe
CORPORATE SOURCE: Imp. Cancer Res. Fund, London, WC2A 3PX, UK
SOURCE: Eukaryotic Viral Vectors, [Conf.] (**1982**), Meeting Date 1981, 29-33. Editor(s): Gluzman, Yakov. Cold Spring Harbor Lab.: Cold Spring Harbor, N. Y.
CODEN: 48DVAI
DOCUMENT TYPE: Conference
LANGUAGE: English
AB The expression of influenza **virus** hemagglutinin encoded by **cDNA** present on SV40 vectors was examined with COS-1 cells as the permissive host; early genes of SV40 were replaced with the **cDNA** , and **vectors** either **contained** or lacked the **intron** of the **SV40** small t antigen gene, inserted between the end of the **coding sequence** for hemagglutinin and the downstream poly(A) addition signal derived from SV40. COS-1 cells were efficient hosts both for the propagation of recombinant hemagglutinin-SV40 genomes and for high-level expression of hemagglutinin. The provision of splice junctions was not required for efficient expression of hemagglutinin. DNA rearrangements rapidly accumulated in the SV40 recombinant containing the intron; by the 4th and 5th passage, the intron-containing stock became essentially noninfections.

=>

---Logging off of STN---

=>

Executing the logoff script...

=> LOG Y

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	218.25	218.46

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	-7.92	-7.92

STN INTERNATIONAL LOGOFF AT 17:36:12 ON 06 JUL 2004